

“t09200t” t4262000t

A

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 QKLI AAQEAQADSQSPKLGCCWPHSLIPARDLQSHRPAI VRRLLSHVENM DLAWERGFVSQYECDEI RLPI FTPSQRARRLDLDATVKANGLAFFLL 200  
 QHVQELPVPALPLEAATCKKYMAKLRTTVSAQSRFLSTYDGAETLCLEDI YTENVLEVWADVGMAGPPQKSPATLGLLEELFSTPGHLNDADITVLVWQE 300  
 AGSGKSTLLQRLHLLWAAGQDFQEFLLFVPFSCRQLQCMAPLSVTRTLFEHCWPDVQEDI FQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP 400  
 TSVQTLFNLQGNLLKNARKVWTSRPAASVAFRLKYIRTEFNLKGFSEQGIELYLRKRHEPGVADRLIRLLQETSALHGLCHLPVFSWWSKCHQELL 500  
 LQEGGSPKTTTDMLLLI LQHFLLHATPPDSASQGLGPSLLRGRLPTLLHLGRALWELGMCCYVFSAAQLQAQVSPDDI SLGFLVRAGVVPGSTAPLE 600  
 FLHI TFQCFFAAFYALASADVPPALLRHLFNCRPGNSPMARLLPTMCI QASEGKDSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQISEKAL 700  
 LRHQACARWCLARSLRKHFHSI PPAAAPGEAKSVHAMPGFI WLIRSLYEMQEERLARKAARGLNVGHLKLTFCSVGPTECAALAFVLQHLRRPVALQLDYN 800  
 SVGDI GVEQLLPCLGVCKALYLRDNNISDRGI CKLIECALHCEQLQKLALFNNKLTGCAHSMAKLLACRQNFALRLGNNTAAAGAQVLAEGLRGNTS 900  
 LQFLGFWGNRVGDEGAQALAEALGDHQLRWLSLVGNNIGSVGAQALALMAKNVM EELCLEENHLQDEGVCSLAEGKKNSLKI LKLSNNCI TYLGA 1000  
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B

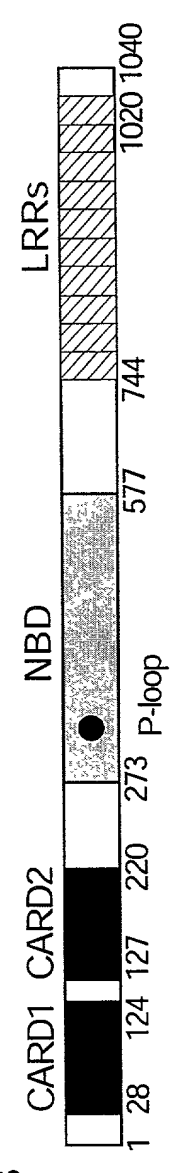
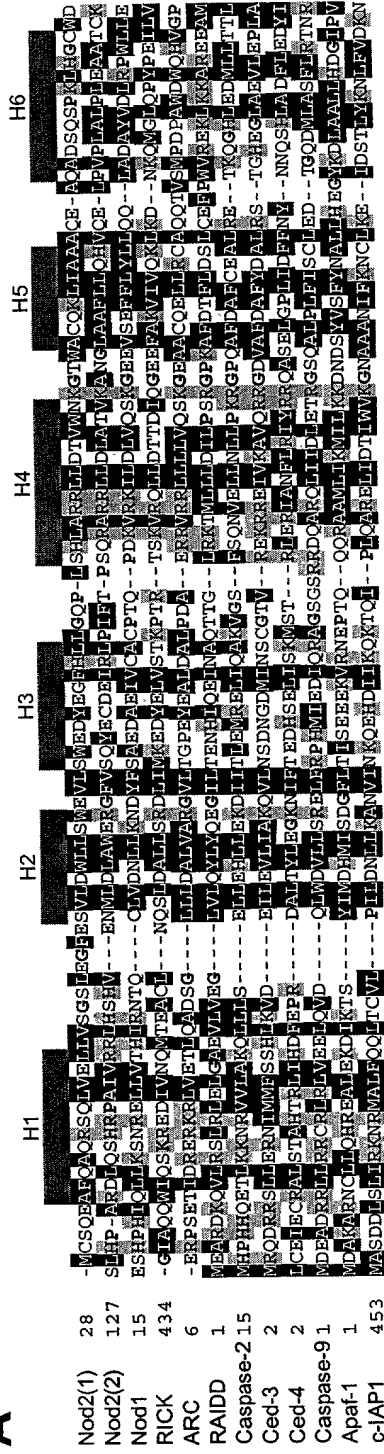
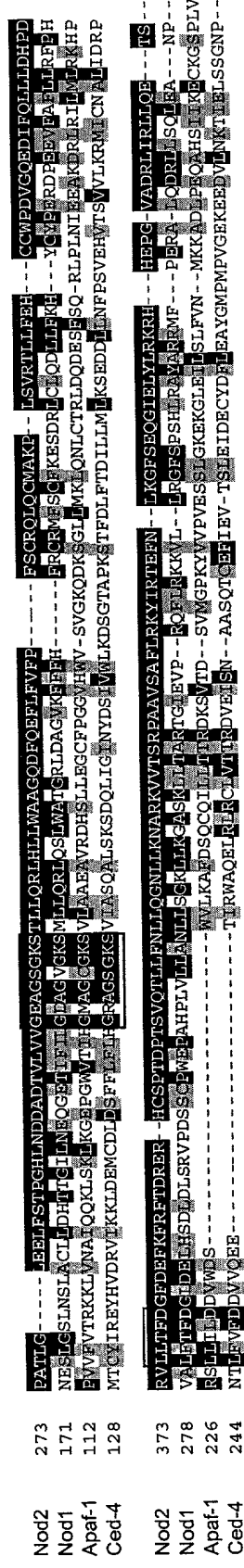


Figure 1

**A**



**B**



**C**

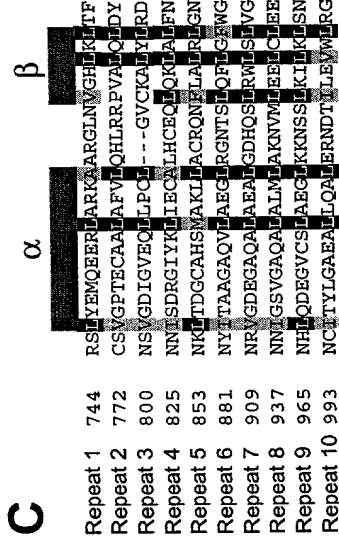


Figure 2

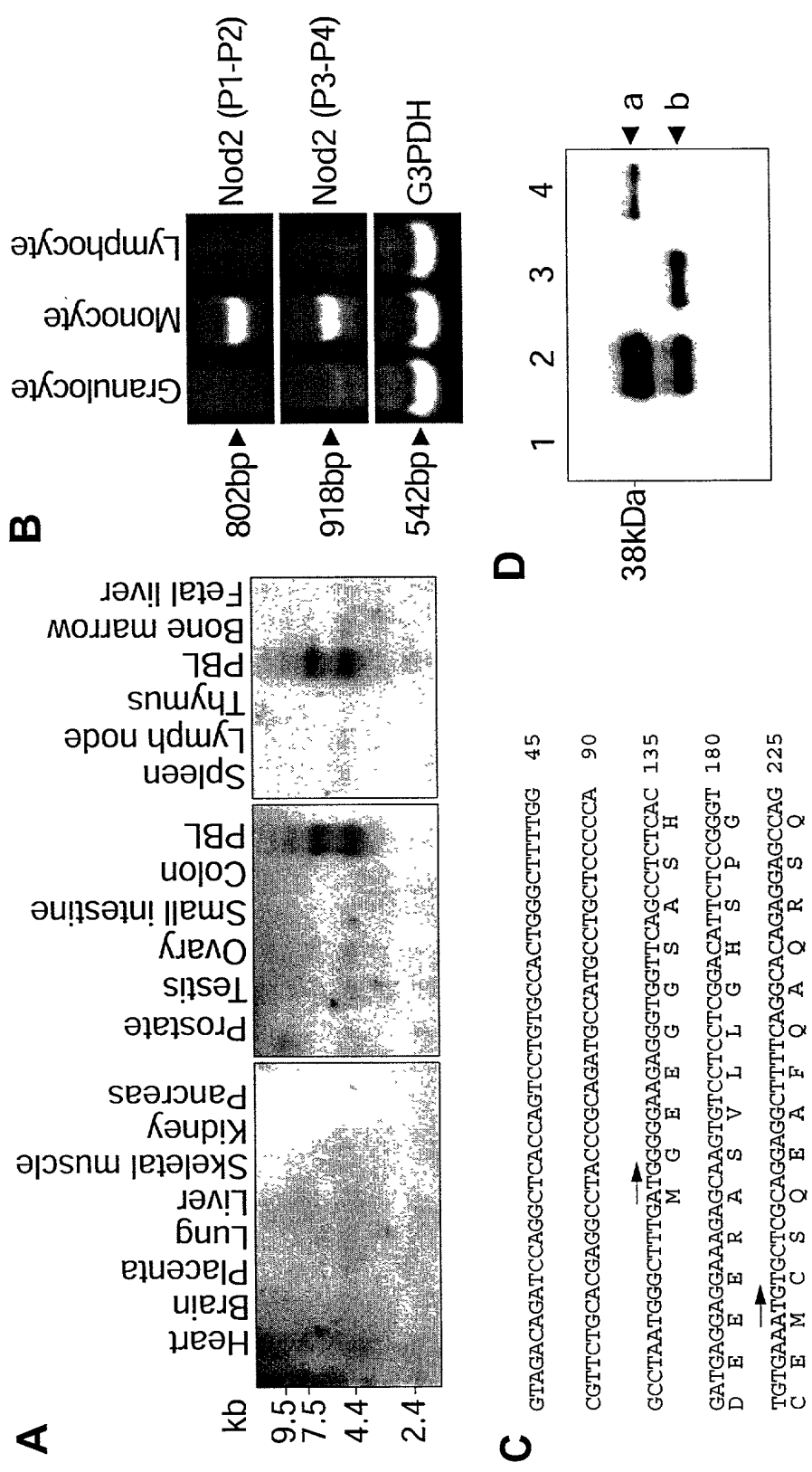


Figure 3

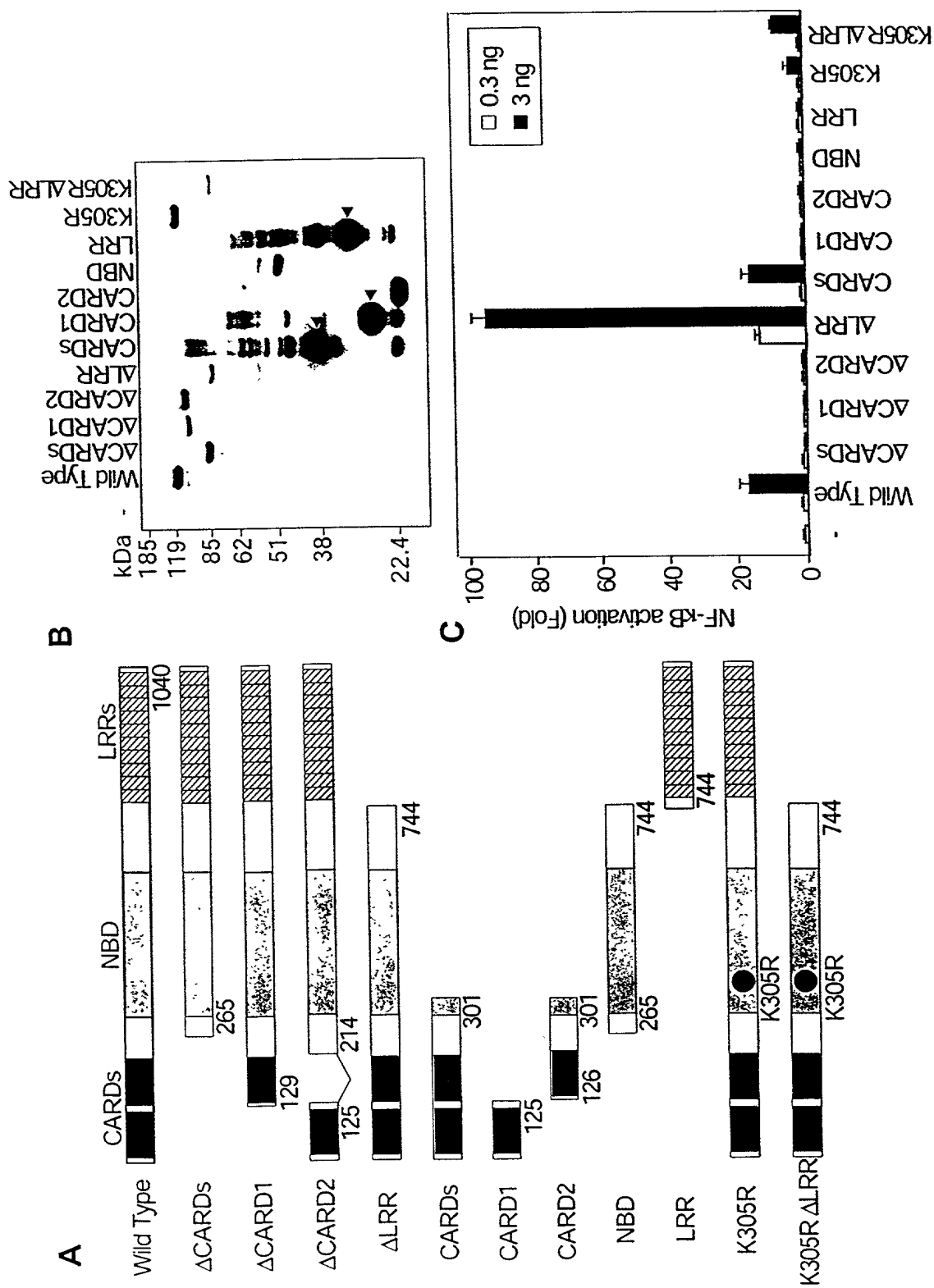


Figure 4

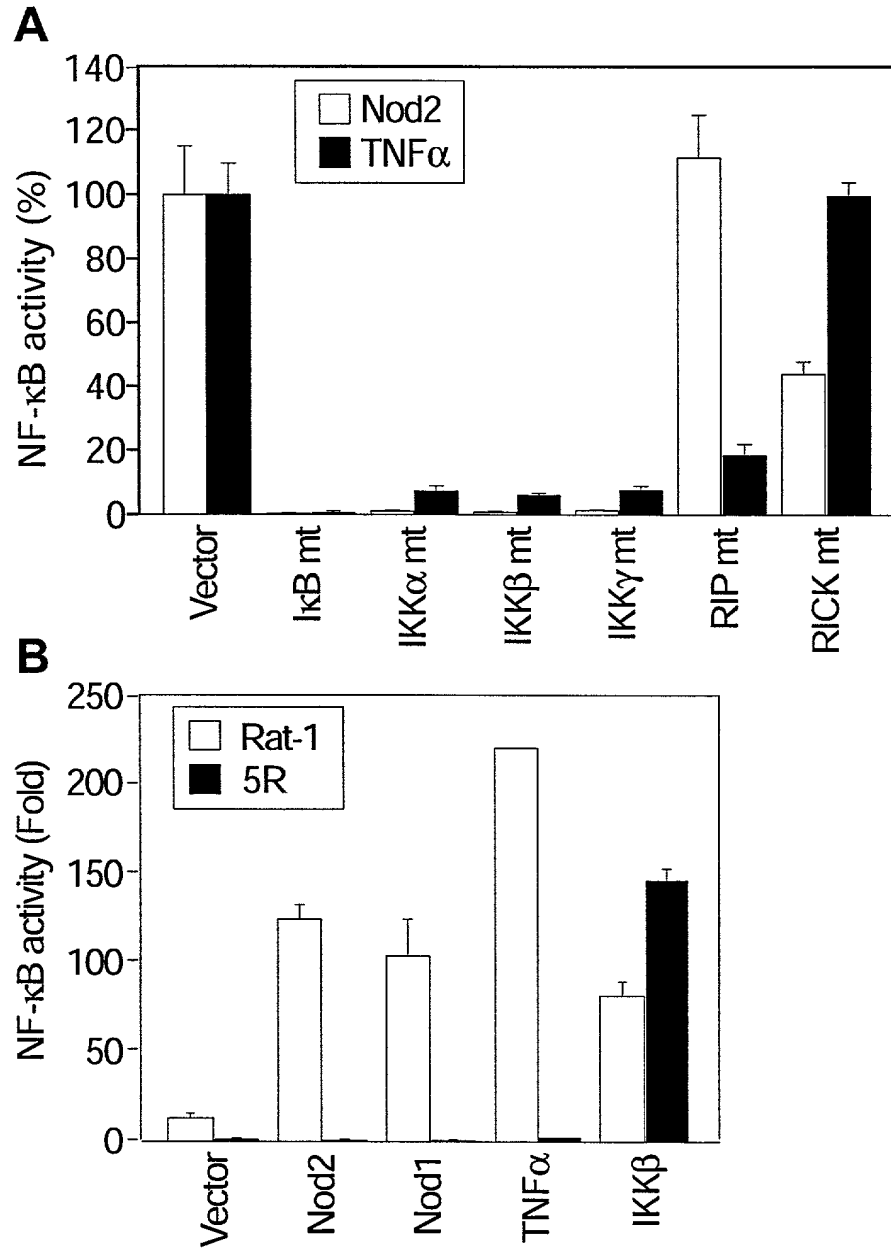
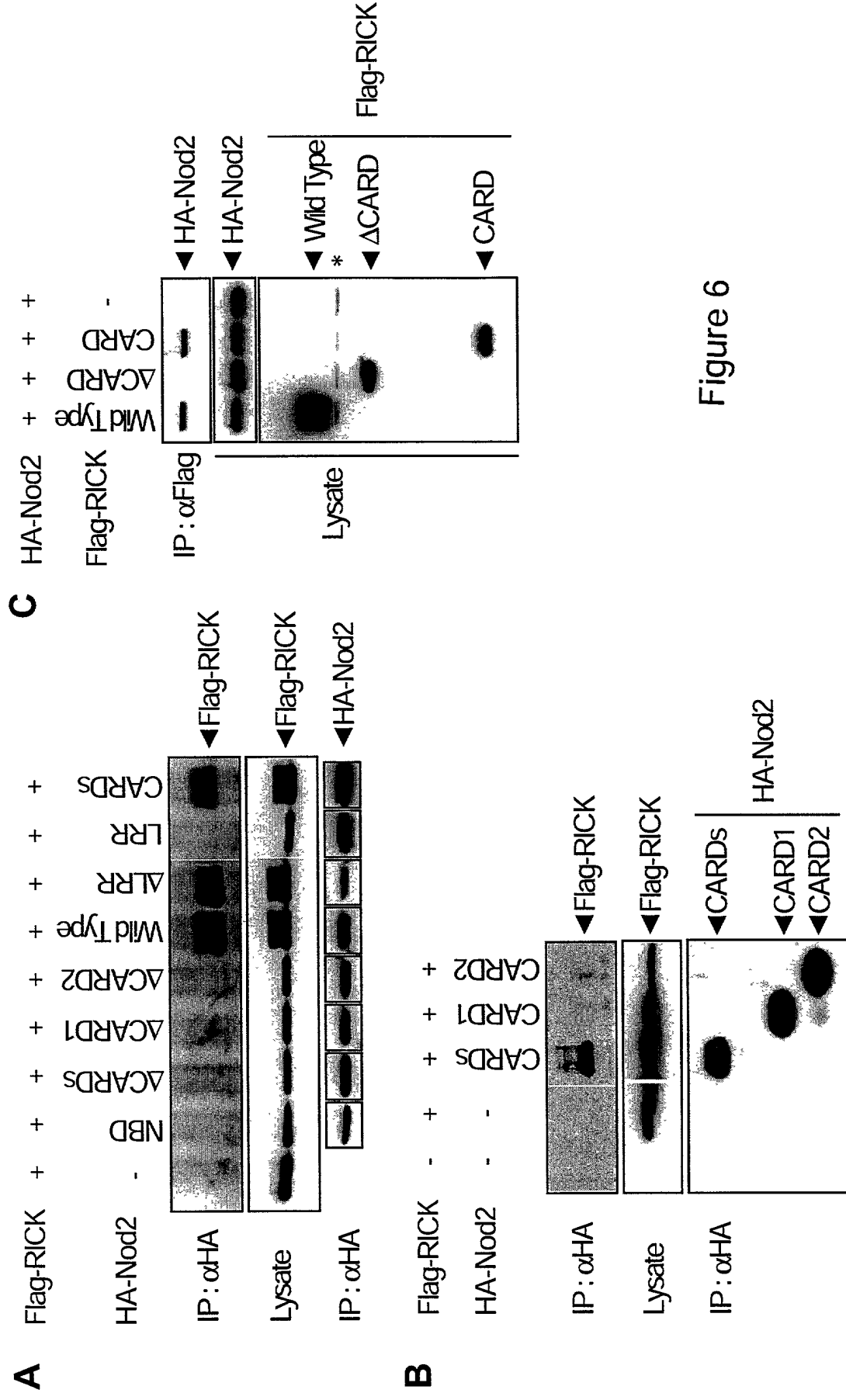


Figure 5



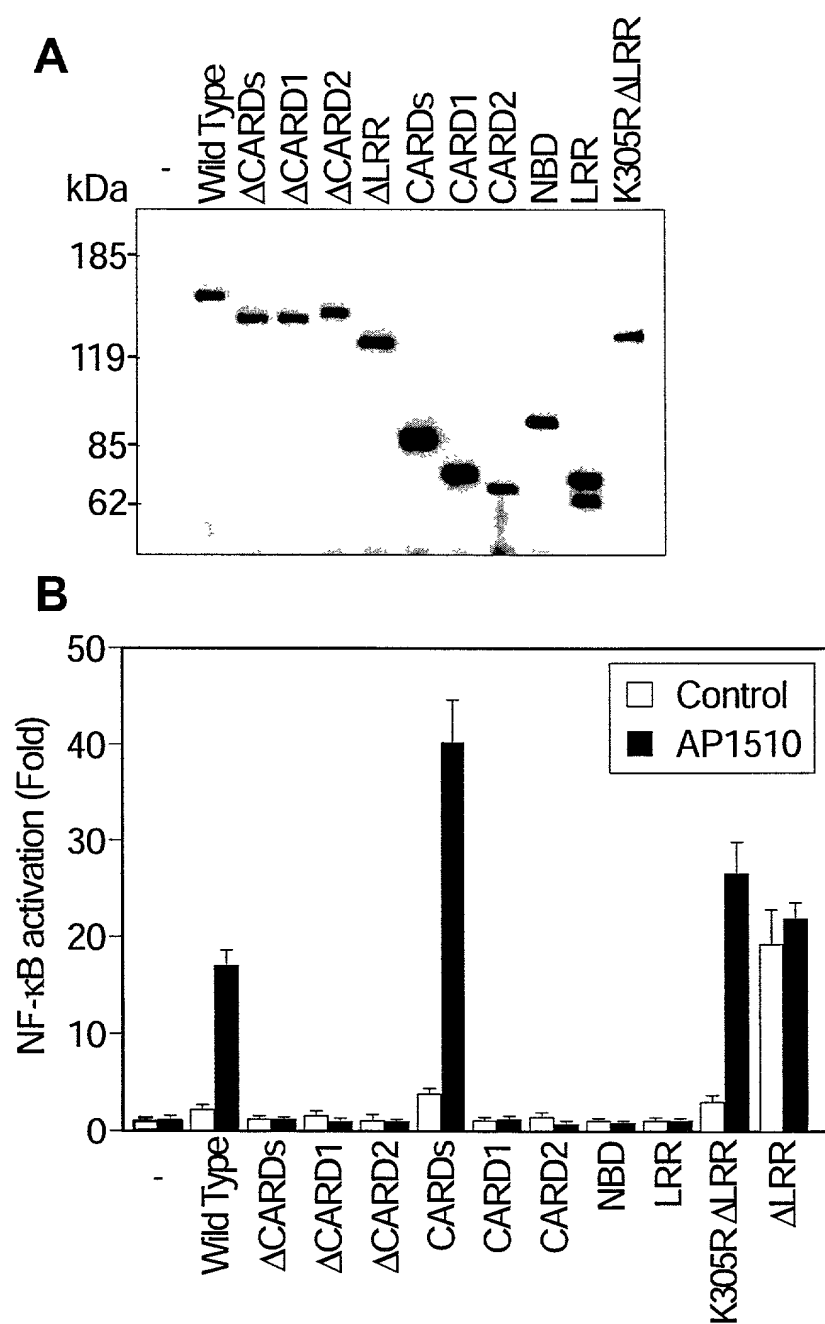
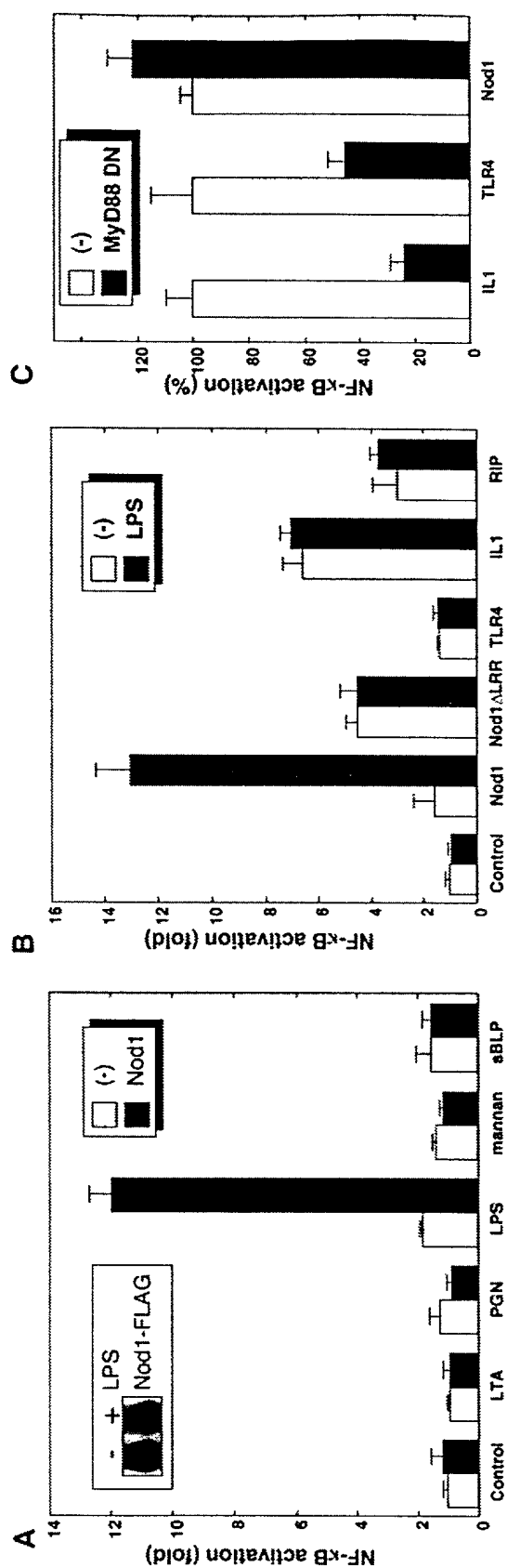


Figure 7



**Figure 8**



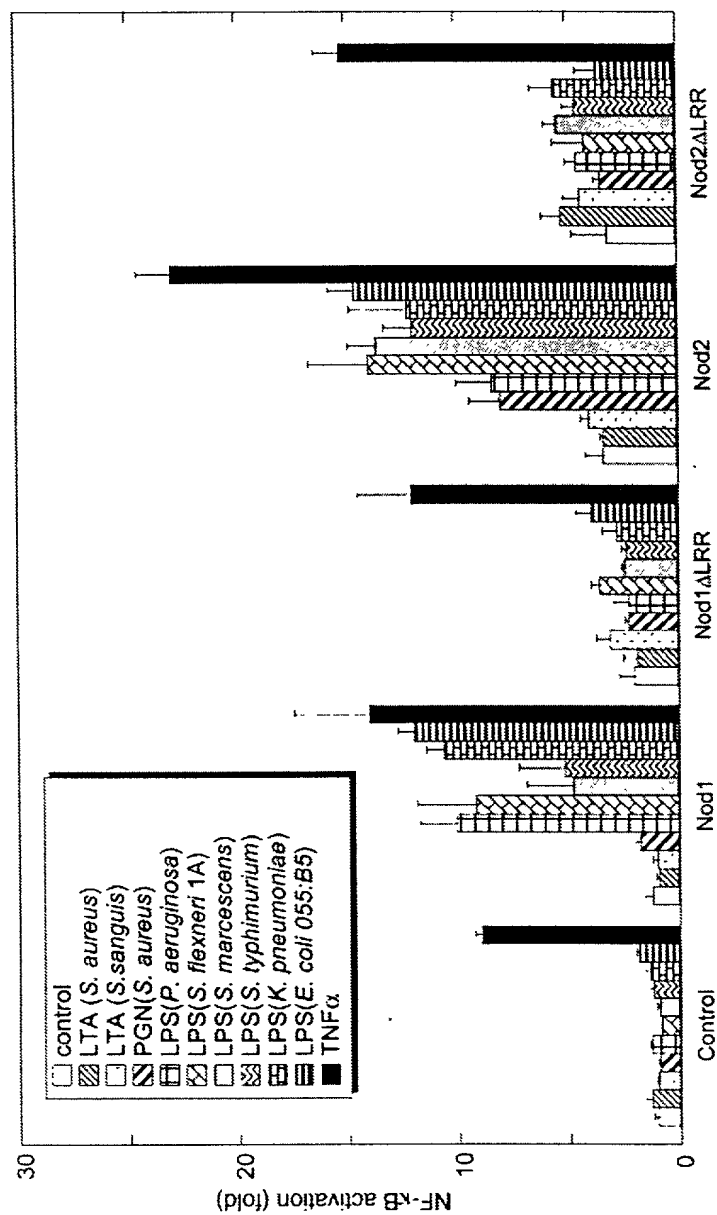
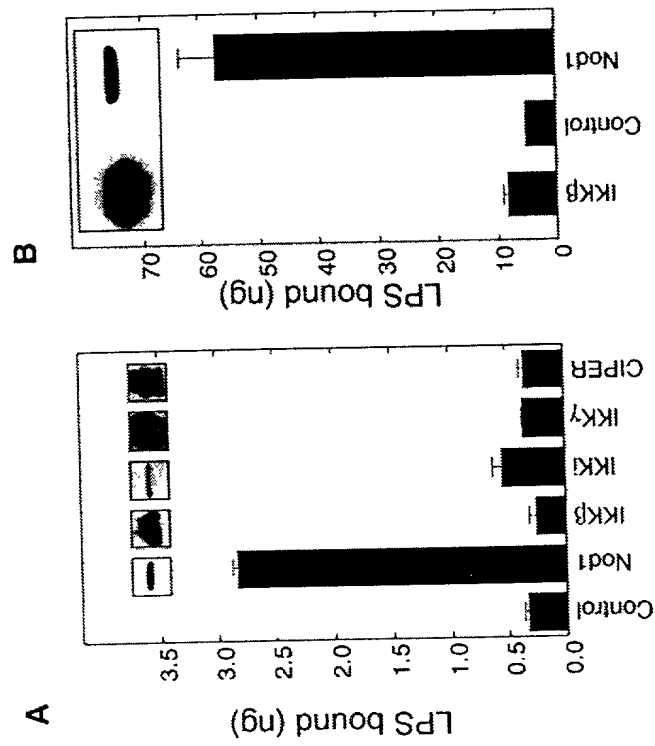


Figure 9



**Figure 10**

# Figure 11

## SEQ ID NO:33

Nod2 cDNA sequence

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tgtgaaatgt gctcgcagga ggcttttcag gcacagagga gccagctggg cgagctgctg	240
gtctcagggt ccttggaagg cttcgagagt gtctggact ggctgctgtc ctgggagggtc	300
ctctcctggg aggactacga gggcttcac ctctggggc agcctctctc ccacttgccc	360
aggcgccctt tggacacgt ctggaataag ggtacttggg cctgtcagaa gctcatcgcg	420
gctgccaag aagcccaggc cgacagccag tcccccaagc tgcattgctg ctgggacccc	480
cactcgtcc acccagccc agacctgcag agtcaccggc cagccattgt caggaggctc	540
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## Figure 12

### SEQ ID NO:1

#### Nod2 cDNA sequence

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# Figure 13

## SEQ ID NO:2

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LSWEVLSWED YEGFHLLGQP LSHLARLLD TVWNKGTWAC QKLIAAAQEA QADSQSPKLH  
GCWDPHSLHP ARDLQSHRPA IVRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTPSQR  
ARRLLDLATV KANGLAAFL L QHVQELPVPL ALPLEAATCK KYMAKLRTTV SAQSRFLSTY  
DGAETLCLED IYTENVLEVW ADVGMAGPPQ KSPATLGLEE LFSTPGHLND DADTVLVVGE  
AGSGKSTLLQ RLHLLWAAGQ DFQEFLLVFP FSCRQLQCMA KPLSVRTLLF EHCCWPDVGQ  
EDIFQLLLDH PDRVLLTFDG FDEFKFRFTD RERHCSPTDP TSVQTLLFNL LQGNLLKNAR  
KVVTSRPAAV SAFLRKYIRT EFNKGFSEQ GIELYLRKRH HEPGVADRLI RLLQETSALH  
GLCHLPVFSW MVSCHQELL LQEGGSPKTT TDMYLLILQH FLLHATPPDS ASQGLGPSLL  
RGRLLPTLLHL GRLALWGLGM CCYVFSQQ L QAAQVSPDDI SLGFLVRAKG VVPGSTAPLE  
FLHITFQCFE AAFYLALSAD VPPALLRHLF NCGRPGNSPM ARLLPTMCIQ ASEGKDSSVA  
ALLQKAEPHN LQITAAFLAG LLSREHWGLL AECQTSEKAL LRRQACARWC LARSLRKHFH  
SIPPAAPGEA KSVHAMPGEI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTCA  
ALAFVLQHLR RPVALQLDYN SVGDIGVEQL LPCLGVCKAL YLRDNNISDR GICKLIECAL  
HCEQLQKLAL FNNKLTGCA HSMALLACR QNFLALRLGN NYITAAGA QV LAEGLRGNTS  
LQFLGFWGNR VGDEGAQALA EALGDHQLR WLSLVGNNIG SVGAQALALM LAKNVMLEEL  
CLEENHLQDE GVCSLAELK KNSSLKILKL SNNCITYLGA EALLQALERN DTILEVWLRG  
NTFSLEEVDK LGCRDTRLLL \*

1002974.102604

## Figure 14

SEQ ID NO:3

MCSQEAFQAQ RSQLVELLVS GSLEGFESVL DWLLSWEVLS WEDYEGFHLL GQPLSHLARR  
LLDTVWNKGT WACQKLIAAA QEAQADSQSP KLHGCWDPHS LHPARDLQSH RPAIVRRRLHS  
HVENMLDLAW ERGFVSQYEC DEIRLPIFTF SQRARRLLDL ATVKANGLAA FLLQHVQELP  
VPLALPLEAA TCKKYMALR TTVSAQSRFL STYDGAETLC LEDIYTENVL EVWADVGMAG  
PPQKSPATLG LEELFSTPGH LNDDADTVLV VGEAGSGKST LLQRLHLLWA AGQDFQEFLF  
VFPFSCRQLQ CMAKPLSVRT LLFEHCCWPD VGQEDIFQLL LDHPDRVLLT FDGFDEFKFR  
FTDRERHCSP TDPTSVQTLL FNLLQGNLLK NARKVVTSRP AAVSAFLRKY IRTEFNLKGF  
SEQGIELYLR KRHHEPGVAD RLIRLLQETS ALHGLCHLPV FSWMVSKCHQ ELLLQEGGSP  
KTTTDMYLLI LQHFL LHATP PDSASQGLGP SLLRGRLPTL LHLGRLALWG LGMCCYVFSA  
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GLLAECQTSE KALLRRQACA RWCLARSLRK HFHSIPPAAP GEAKSVHAMP GFIWLIRSLY  
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EQLLPCLGVC KALYLRDNNI SDRGICKLIE CALHCEQLQK LALFNNKLTG GCAHSMALL  
ACRQNFALR LGNNYITAAG AQVLAEGLRG NTSLQFLGFW GNRVGDEGAQ ALAEALGDHQ  
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100294.10201

**Figure 15**  
**SEQ ID NO:34**

Nod2a AA sequence, Mutant

MGEEGGSASH DEEERASVLL GHSPGCEMCS QEAFQAQRSQ LVELLVSGSL EGFESVLDWL  
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GCWDPHSLHP ARDLQSHRPA IVRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTSPQR  
ARRLLDLATV KANGLAAFL L QHVQELPVPL ALPLEAATCK KYMAKLRTTV SAQSRFLSTY  
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HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGAQV LAEGLRGNTS  
LQFLGFWGNR VGDEGAQALA EALGDHQLR WLSLVGNNIG SVGAQALALM LAKNVMLEEL  
CLEENHLQDE GVCSLAEBLK KNSSLKILKL SNNCITYLGA EALLQAP\*

FIGURE 16

Nod2 Exon11, Wild type

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tatcttcttt tccagGTTGT CCAATAACTG CATCACCTAC CTAGGGGCAG AAGCCCTCCT

L S N N C I T Y L G A E A L L

GCAGGCCCTT GAAAGGAATG ACACCATCCT GGAAGTCTGg taaggcccct gggcaggcct

Q A L E R N D T I L E V

gttttagctc tccgaacctc agtttttcta tctgtaaaat ggggtgacgg gagagaggaa

tggcagaatt ttgaggatcc cttctgattc tgacattcag tgagaatgat tctgcatgtg

Nod2 Exon11, Mutant

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tatcttcttt tccagGTTGT CCAATAACTG CATCACCTAC CTAGGGGCAG AAGCCCTCCT

L S N N C I T Y L G A E A L L

GCAGGCCCTT TGAAAGGAAT GACACCATCC TGGAAGTCTG gtaaggcccc tgggcaggcc

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Q A P \*

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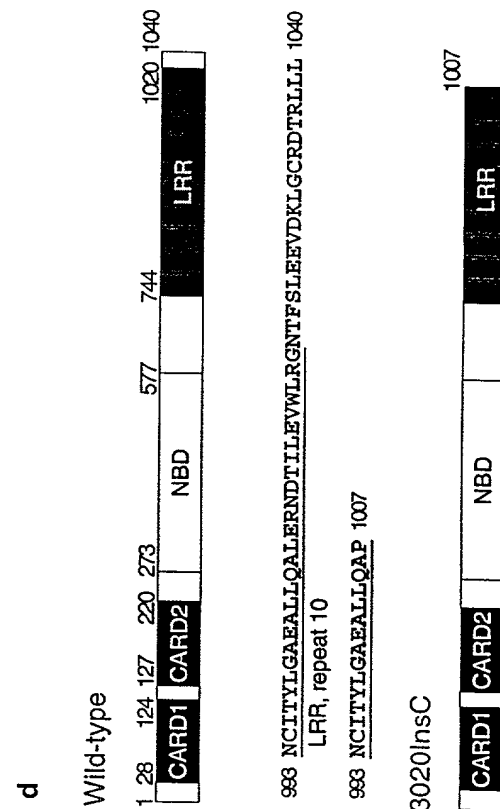
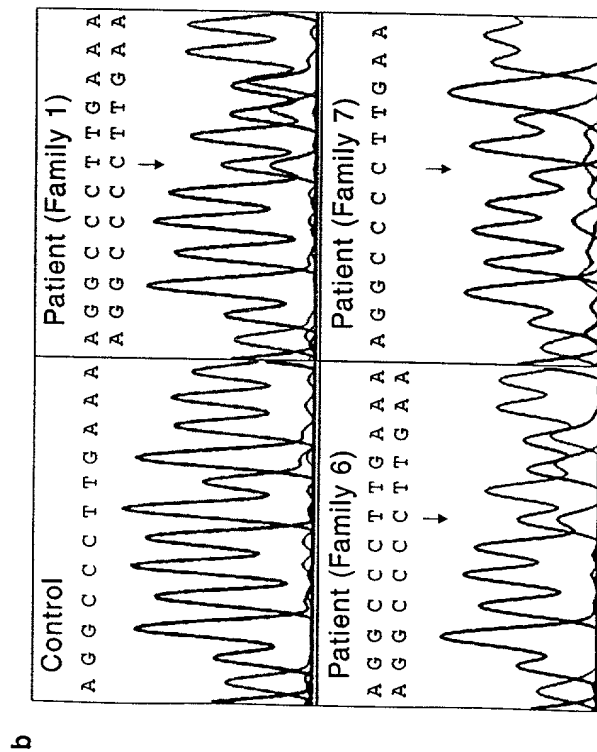
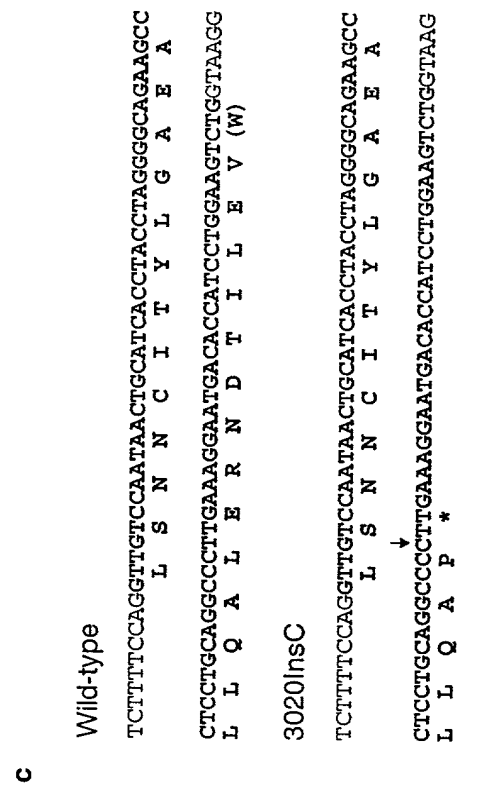
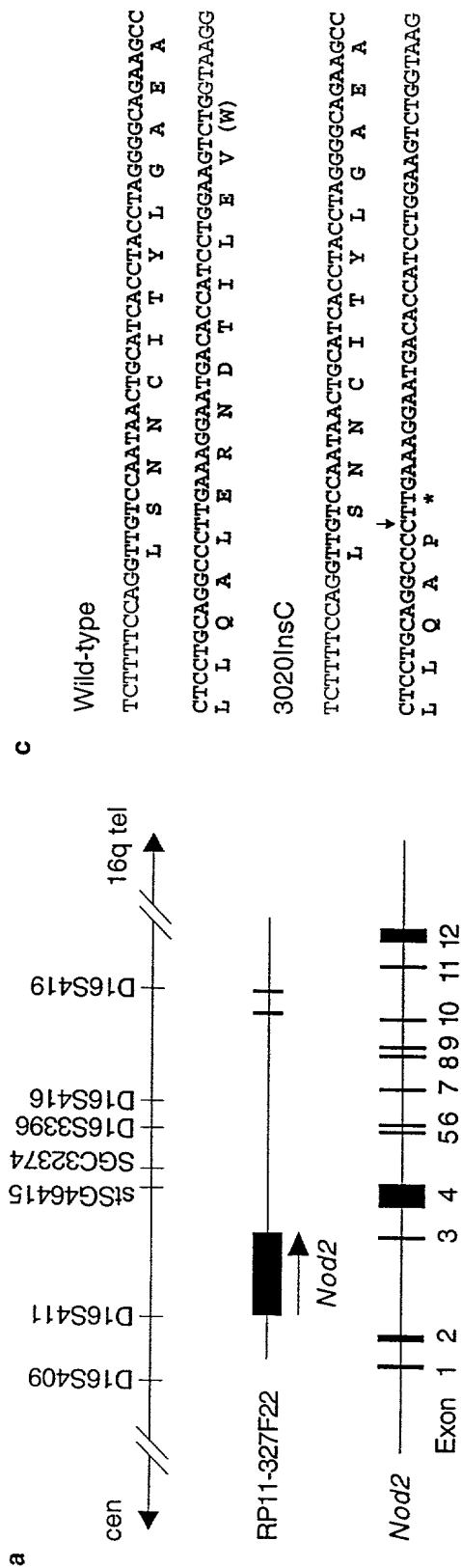
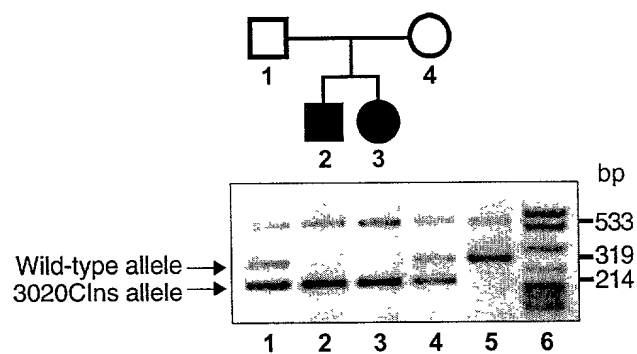
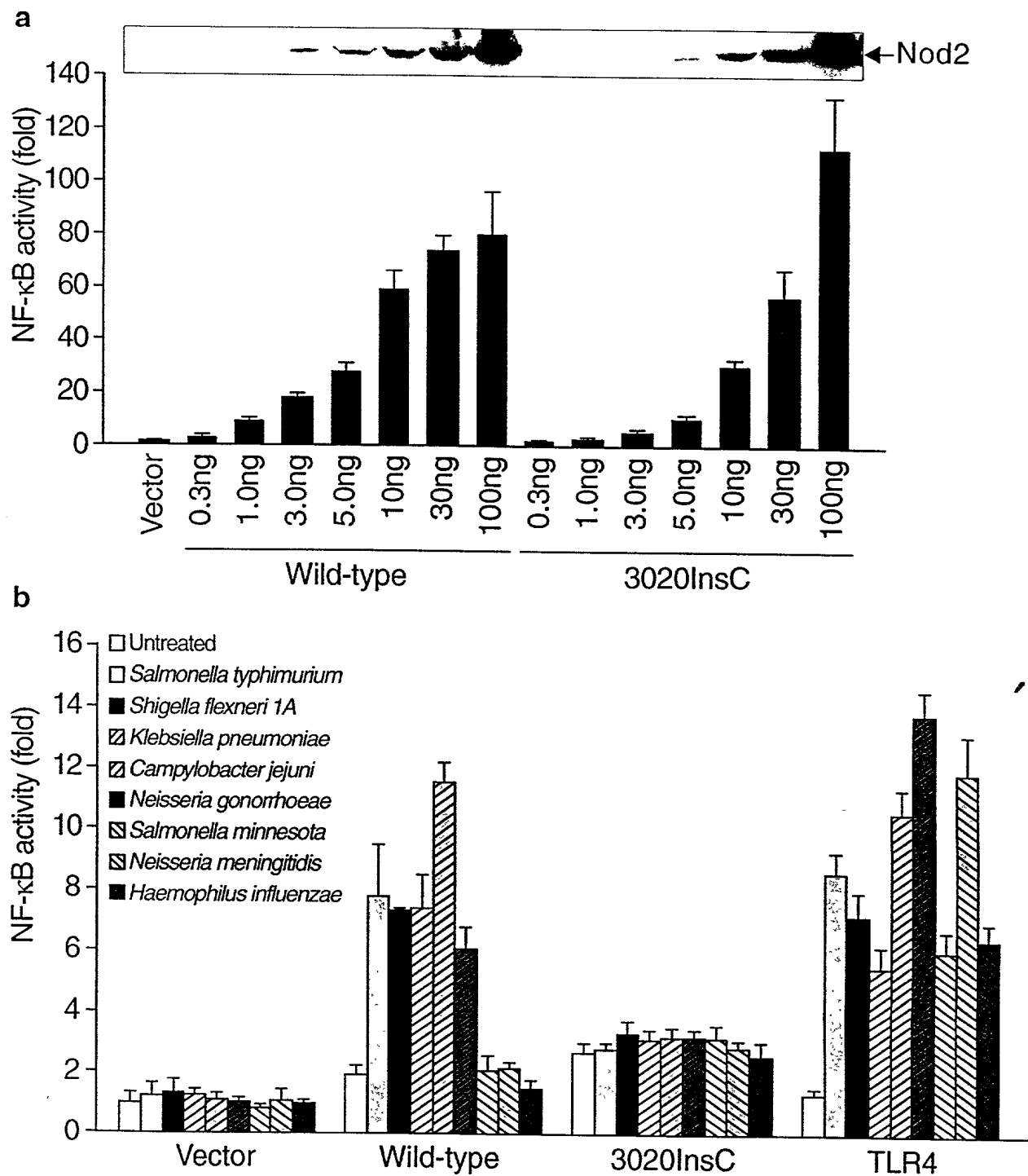


Figure 17



**Figure 18**



**Figure 19**



## Figure 20

### SEQ ID NO: 53

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[illegible][illegible]

## Figure 22

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 180 GCWDPHSLHP ARDLQSHRPA IVRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTPSQR  
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 300 DGAETLCLED IYTENVLEW ADVGMAGSPQ KSPATLGLEE LFSTPGHLND DADTVLVVGE  
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 480 KVVTSRPAAV SAFLRKYIRT EFNKGFSEQ GIELYLRKRH HEPGVADRLI RLLQETSALH  
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 600 RGRLPDLLHL GRLALWGLGM CCYVFSAAQL QAAQVSPDDI SLGFLVRAKG VVPGSTAPLE  
 660 FLHITFQCFE AAFYLALSAD VPPALLRHLE NCRPGNSPM ARLLPTMCIQ ASEGKDSSVA  
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 780 SIPPAAPGEA KSVHAMPFI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTECA  
 840 ALAFVLQHLR RPVALQLDYN SVGDIGVEQL LPCLGVCKAL YLRDNNISDR GICKLIECAL  
 900 HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGAQV LAEGLRGNTS  
 960 LQFLGFWGNR VGDEGAQALA EALGDHQSLR WLSLVGNIG SVGAQALALM LAKNVMLEEL  
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# Figure 23

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# Figure 24

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100294-10001

**Figure 25**  
**SEQ ID NO: 58**

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10002974.102601

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	2	GGCAGATGTGGGCATGGCTGGAICC; SEQ ID NO:71	S		
SNP20	1	AGACATCTGAGAAGGCCCTGCTCCGG; SEQ ID NO:72	R	R 702 W	nt 2104
	2	AGACATCTGAGAAGGCCCTGCTCIGG; Seq ID NO:73	W		
SNP7	1	CTGCAGCACCTCCGGCGGCCCGTG; SEQ ID NO:74	V	V 793 M	nt 2377
	2	CTGCAGCACCTCCGGCGGCCCATG; SEQ ID NO:75	M		
SNP18	1	TTGCAGAAAGTTAGCTCTATTCAAC; SEQ ID NO:76	N	N 852 S	nt 2555
	2	TTGCAGAAAGTTAGCTCTATTCAAGC; SEQ ID NO:77	S		
SNP25	1	ACTGACGGCTGTGCACACTCCATG; SEQ ID NO:78	M	M 863 V	nt 2587
	2	ACTGACGGCTGTGCACACTCCGTG; SEQ ID NO:79	V		
SNP17	1	TGCAGTTCCTGGGATTCTGGGGC; SEQ ID NO:80	G	G 908 R	nt 2722
	2	TGCAGTTCCTGGGATTCTGGCGC; SEQ ID NO:81	R		
SNP23	1	CACTGATGCTGGCAAAGAAGCTC; SEQ ID NO:82	V	V 955 I	nt 2863
	2	CACTGATGCTGGCAAAGAAGACATC; SEQ ID NO:83	I		
3020C ins	1	GGGCAGAAAGCCCTCCTGCAGGCCCT; SEQ ID NO:90	wild-type		nt 3020
	2	GGGCAGAAAGCCCTCCTGCAGGCCCT; SEQ ID NO:91	frameshift mutation	Δ33	
		*Underlined is mutated base			
		*Nucleotide/amino acid numbers designate the positions in Nod2a as reported by Ogura et al. J. Biol. Chem. 276:4812 [2001]			
		AA = amino acid			
		SNP= single nucleotide polymorphism			

Figure 26

[illegible][illegible]

**Figure 27**



[illegible]

\*

Figure 29  
SEQ ID NO: 60

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aatgtgctcgcaggaggcttttcaggcacagaggagccagctgggtcgagctgctgggtctcagggccctggaaggcttcg  
agagtgtcctggactggctgctgtcctgggaggtcctctcctgggaggactacgagggttccacctcctgggcccagcct  
ctctcccacttgccaggcgcttctggacaccgtctggaataagggtaacttgggcctgtcagaagctcatcgcggtgc  
ccaagaagcccaggccgacagccagtcccccaaagctgcatggctgctgggacccccactcgctccacccagcccagacc  
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ttcgtcagccagtatgaatgtgatgaaatcaggttgccgatcttcacaccgtcccagagggaagaaggctgctgatct  
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tggaagctgccacatgcaagaagtatatggccaagctgaggaccaggtgtctgctcagtcctcctcagtacctat  
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tctgttaacctttgatggctttgacgagttcaagttcaggttcacggatcgtgaacgccactgctccccgaccgaccc  
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tgggccccactgagtgtgctgcccctggccttctgtgctgcagcacctccggcgcccggtggcctgcagctggactacaac  
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cctgaagttgtccaataactgcatcacctacctaggggcagaagccctcctgcaggcccttgaaaggaatgacaccatcc  
tggaagtctggctccgaggggaacacttctctctagaggaggttgacaagctcggtgcagggaacaccagactcttgctt  
tga

1002974-102601

**Figure 30**  
**SEQ ID NO: 61**

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFAQRSQVLVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
LSHLARRLLDTVWNKGTWACQKLIAAAQEAQADSQSPKLHGCWDPHSLHPARDLQSHRPAIVRRRLHSHVENMLDLAWERG  
FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLP TLLHLGRLALWGLGM  
CCYVFSQQQLQAAQVSPDDISLGLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIIRSLYEMQEERLARKAARGLNVGHLKLTFCSVGPTCAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMALLACRQNFALRLGN  
NYITAAGAQLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSLRWLSLVGNNIGSVGAQALALMLAKNVMLEEL  
CLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL  
\*

Figure 30

[illegible][illegible]

[illegible]

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Figure 33  
SEQ ID NO: 64

atgggggaagaggggtgggttcagcctctcacgatgaggaggaaagagcaagtgtcctcctcggacattctccgggttgtga  
aatgtgctcgcaggaggcttttcaggcacagaggagccagctggctcgagctgctggctcaggggtccctggaaggcttcg  
agagtgtcctggactggctgctgtcctgggaggtcctcctcctgggaggactacgagggcttcacctcctgggcccagcct  
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ccaagaagcccaggccgacagccagtcacccaagctgcatggctgctgggacccccactcgctccacccagcccagagacc  
tgcagagtacccggccagccattgtcaggaggctccacagccatgtggagaacatgctggacctggcatgggagcgggggt  
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aaagaccactacagatatgtacctgctgattctgcagcatttctgctgcagccccccagactcagcttcccaag  
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tggaagtctggctccgaggggaacacttctctctagaggaggttgacaagctcggctgcagggaacaccagactcttgctt  
tga

1002974.102601

**Figure 34**  
**SEQ ID NO: 65**

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVLELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
LSHLARRLLDTVWNKGTWACQKLIAAAQEAQADSQSPKLHGCWDPHSLHPARDLQSHRPAIVRRLHSHVENMLDLAWERG  
FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVEPVPPLALPLEAATCKKYMALRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHPEPGVADRLIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLLPTLLHLGRLLWGLGM  
CCYVFSQQQLQAAQVSPDDISLGFLVRAGVVPGSTAPLEFLHITFQCFFAAFYLALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLVNHLKLTFCVGPTECAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFSNKLTDGCAHSMAKLLACRQNFALRLGN  
NYITAAGAQLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQLRWLSLVGNNIGSVGAQALALMLAKNVMLEEL  
CLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL

\*

100224.102601

# Figure 35

## SEQ ID NO: 66

atgggggaagaggggtgggttcagcctctcacgatgaggaggaaagagcaagtgtcctcctcggacattctccgggttgatga  
aatgtgctcgcaggaggtttttcaggcacagaggagccagctggtcgcagctgctggtctcagggtccctggaaggcttcg  
agagtgtcctggactggctgctgtcctgggaggtcctcctcctgggaggactacgagggcttccacctcctgggcccagcct  
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tggaagtctggctccgaggggaacacttctctctagaggaggttgacaagctcggctgcagggaaccagactcttgctt  
tga

1002974.102601



**Figure 36**  
**SEQ ID NO: 67**

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFAQRSQVLVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
LSHLARRLLDTVWNKGTWACQKLIAAAQEAQADSQSPKLHGCWDPHSLHPARDLQSHRPAIVRRLHSHVENMLDLAWERG  
FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQLHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLLPTLLHLGRLALWGLGM  
CCYVFSAAQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCVSGPTECAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMAKLLACRQNFLALRLGN  
NYITAAGAQLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSRLWLSLVGNNIGSVGAQALALMLAKNIMLEEL  
CLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLILL  
\*

1000224-10001

Figure 37  
SEQ ID NO: 68

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gacttccaggaatttctctttgtcttccattcagctgccggcagctgcagtgcattggccaaacctctctgtgcggac  
tctactctttgagcactgctgttggtgatgttggtcaagaagacatcttccagttactccttgaccacctgaccgtg  
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cctgaagttgtccaataactgcatcacctacctaggggcagaagccctcctgcaggcccttgaaaggaatgacaccatcc  
tggaagtctggctccgaggggaacacttctctctagaggaggttgacaagctcggctgcagggaacaccagactcttgctt  
tga

[illegible]

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**Figure 39**  
**SEQ ID NO: 84**

atgggggaagaggggtggttcagcctctcacgatgaggaggaaagagcaagtgtcctcctcggaacattctccgggttggtga  
aatgtgctcgcaggaggcttttcaggcacagaggagccagctggtcgagctgctggtctcaggggtccctggaaggcttcg  
agagtgtcctggactggctgctgtcctgggaggtcctctcctgggaggactacgaggggttccacctcctgggccagcct  
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gatggagcagagacgctctgcctggaggacatatacacagagaatgtcctggaggtctgggcagatgtgggcagtggtgg  
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gacttccaggaatttctcttcttcttccattcagctgcccgcagctgcagtgcagtgccaaaccactctctgtgcggac  
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tctgttaacctttgatggctttgacgagttcaagttcaggttcacggatcgtgaacgccactgctccccgaccgacccc  
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tgccctggaggagaacctctccaggatgaagggtgatgttctctgcagaaggactgaagaaaaattcaagtttgaaaat  
cctgaagttgtccaataactgcatacctacctaggggcagaagccctcctgcaggcccttgaaaggaatgacaccatcc  
tggaagtctggctccgagggaacacttctctctagaggaggttgacaagctcggtgcagggaacaccagactcttgctt  
tga

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**Figure 40**  
**SEQ ID NO: 85**

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQLVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
LSHLARRLLDTVWNKGTWACQKLIAAAQEAQADSQSPKLHGCWDPHSLHPARDLQSHRPAIVRRRLHSHVENMLDLAWERG  
FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVVQELPVPLALPLEAATCKKYMALRRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLKRHHHEPGVADRILIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLPDLLHLGRLLALWGLGM  
CCYVFSQQQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAYLALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFILWIRSLYEMQEERLARKAARGLNVGHLKLTFCVGPTECAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNKLTDCGAHSMALLACRQNFALRLGN  
NYITAAGAQLAEGLRGNTSLQFLGFWRNRVGDEGAQALAEALGDHQSRLWLSLVGNNIGSVGAQALALMLAKNVMLEEL  
CLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL  
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**Figure 42**  
**SEQ ID NO: 87**

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
LSHLARRLLDTVWNKGTWACQKLI AAAQEAQADSQSPKLHGCWDPHSLHPARDLQSHRPAIVRRLHSHVENMLDLAWERG  
FVSQYECDEIRLP IFTPSQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMAKLR TTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEF LFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVT SRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADR LI RLLQETSALH  
GLCHLPVFSWMVSKCHQELLLQEGGSPKTTTDMYLLILQHFL LHATPPDSASQGLGPSLLRGRLPTLLHLGRLALWGLGM  
CCYVFS AQQLQAAQVSPDDISLGFLVRAGVVP GSTAPLEFLHITFQCFFAAFYLALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFC SVGPTCAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFSNKLT DGC AHSMAKLLACRQNFLALRLGN  
NYITAAGAQVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSRLWLSLVGN NIGSVGAQALALMLAKNVMLEEL  
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[illegible]

tga



**Figure 44**  
**SEQ ID NO: 89**

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFAQRSQLVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
LSHLARRLLDTVWNKGTWACQKLIAAAQEAQADSQSPKLHGCWDPHSLHPARDLQSHRPAIVRRLHSHVENMLDLAWERG  
FVSQYECDEIRLPIFTPSQRARRLLDLATVKANGLAAFLLOHVQELPVPLALPLEAATCKKYMALRRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRILIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLPTLLHLGRLALWGLGM  
CCYVFSQQQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLWRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCVSGPTECAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLDRNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMALLACRQNFALRLGN  
NYITAAGAQVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSRLWLSLVGNNIGSVGAQALALMLAKNVMLEEL  
CLEENHLQDEGVCSLAEGCLKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL  
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